SUBSTITUTE SEQUENCE LISTING

<110> BLUMENFELD, Marta
      BOUGUELERET, Lydie
      CHUMAKOV, Ilya
      COHEN, Daniel
      ESSIOUX, Laurent

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<141> 1999-10-12

<150> 60/106,457

<151> 1999-10-30

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<151> 1998-10-12

<150> 60/132,277

<151> 1999-05-03

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SEQUENCE LISTING

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<120> Genes, proteins and biallelic markers related to central...

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8

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10

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11

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24

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ggaggaggag gggaggcgct ccgggcgccg tcagtgggca gcggaggcgc ggcatgcccc      180
tggcagggga gagcgggctg ggctccgcgg ggccatgggg acccgcgcgc tgacaatgcc      240
tgggtggccg gagccgcgcc agccaccctg tcacctccac catcgccccc tgcacccagc      300
ctcgccgccg gccaccagca ccagcctcct ccgtctctct ctctctctct ctctccatta      360
ttgtttccca ctctacagag gatggggtcg gctgatgatt aggaagcaag tcagaccttc      420
cttcaaagcc tggtaatatt tatgtaggca aaagagacag agagagataa aagagaggga      480
gagggagaga gagagagagg agagagggag aggggaagag agagaaagag agagaggaga      540
gagaaaaaac gggaggaggg gataaggaaa ttaaaccctt taagtcaatg catattgtgg      600
tgacaccggc acaggcgccc tcacggtgga gtcggccagg gctgtgcgtt cccaaaat       658
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atg acc agg ggt gct tgg atg tgt cgg cag tat gac gac ggc tta aaa      706
Met Thr Arg Gly Ala Trp Met Cys Arg Gln Tyr Asp Asp Gly Leu Lys
1               5                   10                  15
atc tgg ttg gca gca ccc cga gag aac gag aaa ccg ttc atc gat tcc      754
Ile Trp Leu Ala Ala Pro Arg Glu Asn Glu Lys Pro Phe Ile Asp Ser
            20                  25                  30
gag agg gct cag aaa tgg cga ctg tct ctg gca tct ctc ttg ttt ttc      802
Glu Arg Ala Gln Lys Trp Arg Leu Ser Leu Ala Ser Leu Leu Phe Phe
        35                  40                  45
aca gtc ctg ctc tct gat cac ttg tgg ttc tgc gcc gag gcc aag ctg      850
Thr Val Leu Leu Ser Asp His Leu Trp Phe Cys Ala Glu Ala Lys Leu
    50                  55                  60
acc cgg gcc cgg gac aag gag cac cag cag cag cag cgg cag cag cag      898
Thr Arg Ala Arg Asp Lys Glu His Gln Gln Gln Gln Arg Gln Gln Gln
65                  70                  75                  80
cag cag cag cag cag cag agg cag cgg cag cag cag cag cag cag cgg      946
Gln Gln Gln Gln Gln Gln Arg Gln Arg Gln Gln Gln Gln Gln Gln Arg
            85                  90                  95
cgg cag cag gag ccc tcc tgg ccc gcg ctc ctg gcg agc atg ggg gag      994
Arg Gln Gln Glu Pro Ser Trp Pro Ala Leu Leu Ala Ser Met Gly Glu
            100                 105                 110
tcc tcg ccc gcc gcc cag gca cac aga ctc ctc tcc gcc tcc tcg tcc      1042
Ser Ser Pro Ala Ala Gln Ala His Arg Leu Leu Ser Ala Ser Ser Ser
            115                 120                 125
ccc acc ctg ccc ccc tcc ccg gga gac ggc ggc ggc ggc ggc ggc aag      1090
Pro Thr Leu Pro Pro Ser Pro Gly Asp Gly Gly Gly Gly Gly Gly Lys
    130                 135                 140
ggc aac cga ggc aaa gac gac cgg ggc aag gct ctt ttt cta gga aac      1138
Gly Asn Arg Gly Lys Asp Asp Arg Gly Lys Ala Leu Phe Leu Gly Asn
145                 150                 155                 160
tct gcc aag ccc gtg tgg cgc ctg gag act tgt tac ccc cag ggc gcg      1186
Ser Ala Lys Pro Val Trp Arg Leu Glu Thr Cys Tyr Pro Gln Gly Ala
            165                 170                 175
tcc tcg ggc cag tgc ttc acg gtg gag aat gcg gac gcg gtg tgc gcc      1234
Ser Ser Gly Gln Cys Phe Thr Val Glu Asn Ala Asp Ala Val Cys Ala
            180             .   185                 190
agg aac tgg agt cgg ggg gcg gcc ggg ggg gac ggg cag gag gtg agg      1282
Arg Asn Trp Ser Arg Gly Ala Ala Gly Gly Asp Gly Gln Glu Val Arg
            195                 200                 205
agc aag cat ccc act ccg ctc tgg aac ttg tcg gat ttt tac ctt tcg      1330
Ser Lys His Pro Thr Pro Leu Trp Asn Leu Ser Asp Phe Tyr Leu Ser
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ttt tgt aat tcc tac aca ctt tgg gag ttg ttc tcg ggg ttg tcc agt      1378
Phe Cys Asn Ser Tyr Thr Leu Trp Glu Leu Phe Ser Gly Leu Ser Ser
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25

ccc aac act ttg aac tgc agt ctg gat gtg gtg ctc aag gaa ggc ggc   1426
Pro Asn Thr Leu Asn Cys Ser Leu Asp Val Val Leu Lys Glu Gly Gly
                245   250   255
gag atg acc act tgc agg cag tgc gtc gag gct tac cag gac tat gac   1474
Glu Met Thr Thr Cys Arg Gln Cys Val Glu Ala Tyr Gln Asp Tyr Asp
                260   265   270
cac cat gct cag gag aaa tac gaa gag ttt gaa agc gtg ctc cac aaa   1522
His His Ala Gln Glu Lys Tyr Glu Glu Phe Glu Ser Val Leu His Lys
                275   280   285
tat tta cag tcg gag gag tac tcg gtg aaa tcc tgt cct gaa gac tgt   1570
Tyr Leu Gln Ser Glu Glu Tyr Ser Val Lys Ser Cys Pro Glu Asp Cys
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aag att gtc tac aaa gcc tgg ctc tgt tcc cag tat ttt gaa gtc aca   1618
Lys Ile Val Tyr Lys Ala Trp Leu Cys Ser Gln Tyr Phe Glu Val Thr
305   310   315   320
cag ttt aac tgc aga aag aca att cct tgc aag caa tac tgt ttg gag   1666
Gln Phe Asn Cys Arg Lys Thr Ile Pro Cys Lys Gln Tyr Cys Leu Glu
                325   330   335
gtt cag acg agg tgt cca ttt ata ttg ccc gac aat gat gaa gtc atc   1714
Val Gln Thr Arg Cys Pro Phe Ile Leu Pro Asp Asn Asp Glu Val Ile
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tac gga ggc ctc tcc agt ttc atc tgt aca ggg ctt tat gaa acc ttt   1762
Tyr Gly Gly Leu Ser Ser Phe Ile Cys Thr Gly Leu Tyr Glu Thr Phe
                355   360   365
cta acc aat gat gaa cca gaa tgc tgt gac gtc agg aga gaa gaa aaa   1810
Leu Thr Asn Asp Glu Pro Glu Cys Cys Asp Val Arg Arg Glu Glu Lys
                370   375   380
tca aat aac cca tcc aaa ggg acc gta gag aaa agt ggc tcc tgt cac   1858
Ser Asn Asn Pro Ser Lys Gly Thr Val Glu Lys Ser Gly Ser Cys His
385   390   395   400
agg aca tcg ctc aca gtg tca tca gca aca aga ctg tgc aac agc aga   1906
Arg Thr Ser Leu Thr Val Ser Ser Ala Thr Arg Leu Cys Asn Ser Arg
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ctc aag ctg tgt gtt ctt gta ctg att ctc tta cac aca gtg ctc aca   1954
Leu Lys Leu Cys Val Leu Val Leu Ile Leu Leu His Thr Val Leu Thr
                420   425   430
gcc tcg gca gca cag aac aca gcc gga ctg agc ttt gga ggc atc aac   2002
Ala Ser Ala Ala Gln Asn Thr Ala Gly Leu Ser Phe Gly Gly Ile Asn
                435   440   445
acg ctg gaa gaa aac tca acc aat gag gag taa cggaaggacg agtgtcacca   2055
Thr Leu Glu Glu Asn Ser Thr Asn Glu Glu *
                450   455
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26

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aatatacaca attttattcc agtatttccc taacatatgg tttaaaatta ttccaggtat     3255
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27

<400> 5

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Glu Arg Ala Gln Lys Trp Arg Leu Ser Leu Ala Ser Leu Leu Phe Phe
        35                  40                  45
Thr Val Leu Leu Ser Asp His Leu Trp Phe Cys Ala Glu Ala Lys Leu
    50                  55                  60
Thr Arg Ala Arg Asp Lys Glu His Gln Gln Gln Gln Arg Gln Gln Gln
65                  70                  75                  80
Gln Gln Gln Gln Gln Gln Arg Gln Arg Gln Gln Gln Gln Gln Arg
                85                  90                  95
Arg Gln Gln Glu Pro Ser Trp Pro Ala Leu Leu Ala Ser Met Gly Glu
        100                 105                 110
Ser Ser Pro Ala Ala Gln Ala His Arg Leu Leu Ser Ala Ser Ser Ser
        115                 120                 125
Pro Thr Leu Pro Pro Ser Pro Gly Asp Gly Gly Gly Gly Gly Gly Lys
    130                 135                 140
Gly Asn Arg Gly Lys Asp Asp Arg Gly Lys Ala Leu Phe Leu Gly Asn
145                 150                 155                 160
Ser Ala Lys Pro Val Trp Arg Leu Glu Thr Cys Tyr Pro Gln Gly Ala
                165                 170                 175
Ser Ser Gly Gln Cys Phe Thr Val Glu Asn Ala Asp Ala Val Cys Ala
            180                 185                 190
Arg Asn Trp Ser Arg Gly Ala Ala Gly Gly Asp Gly Gln Glu Val Arg
            195                 200                 205
Ser Lys His Pro Thr Pro Leu Trp Asn Leu Ser Asp Phe Tyr Leu Ser
    210                 215                 220
Phe Cys Asn Ser Tyr Thr Leu Trp Glu Leu Phe Ser Gly Leu Ser Ser
225                 230                 235                 240
Pro Asn Thr Leu Asn Cys Ser Leu Asp Val Val Leu Lys Glu Gly Gly
                245                 250                 255
Glu Met Thr Thr Cys Arg Gln Cys Val Glu Ala Tyr Gln Asp Tyr Asp
            260                 265                 270
His His Ala Gln Glu Lys Tyr Glu Glu Phe Glu Ser Val Leu His Lys
        275                 280                 285
Tyr Leu Gln Ser Glu Glu Tyr Ser Val Lys Ser Cys Pro Glu Asp Cys
    290                 295                 300
Lys Ile Val Tyr Lys Ala Trp Leu Cys Ser Gln Tyr Phe Glu Val Thr
305                 310                 315                 320
Gln Phe Asn Cys Arg Lys Thr Ile Pro Cys Lys Gln Tyr Cys Leu Glu
                325                 330                 335
Val Gln Thr Arg Cys Pro Phe Ile Leu Pro Asp Asn Asp Glu Val Ile
            340                 345                 350
Tyr Gly Gly Leu Ser Ser Phe Ile Cys Thr Gly Leu Tyr Glu Thr Phe
        355                 360                 365
Leu Thr Asn Asp Glu Pro Glu Cys Cys Asp Val Arg Arg Glu Glu Lys
    370                 375                 380
Ser Asn Asn Pro Ser Lys Gly Thr Val Glu Lys Ser Gly Ser Cys His
385                 390                 395                 400
Arg Thr Ser Leu Thr Val Ser Ser Ala Thr Arg Leu Cys Asn Ser Arg
                405                 410                 415
Leu Lys Leu Cys Val Leu Val Leu Ile Leu Leu His Thr Val Leu Thr
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                    420                   425                   430
Ala Ser Ala Ala Gln Asn Thr Ala Gly Leu Ser Phe Gly Gly Ile Asn
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Thr Leu Glu Glu Asn Ser Thr Asn Glu Glu
      450                   455


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<211> 1791
<212> DNA
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                                                          Met Thr Arg
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ggt gct tgg atg tgt cgg cag tat gac gac ggc tta aaa atc tgg ttg       106
Gly Ala Trp Met Cys Arg Gln Tyr Asp Asp Gly Leu Lys Ile Trp Leu
      5                   10                  15
gca gca ccc cgg gag aac gag aaa ccg ttc atc gat tca gag cgg gct      154
Ala Ala Pro Arg Glu Asn Glu Lys Pro Phe Ile Asp Ser Glu Arg Ala
20                  25                  30                  35
cag aaa tgg cga ctg tct ctg gct tct ctc ttg ttt ttc aca gtc ctg      202
Gln Lys Trp Arg Leu Ser Leu Ala Ser Leu Leu Phe Phe Thr Val Leu
                  40                  45                  50
ctc tct gat cac ttg tgg ttc tgc gcc gag gcc aag ctg acc cgg acc      250
Leu Ser Asp His Leu Trp Phe Cys Ala Glu Ala Lys Leu Thr Arg Thr
              55                  60                  65
cgg gac aaa gag cat cac caa cag cag cag caa cag cag caa cag cag      298
Arg Asp Lys Glu His His Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln
              70                  75                  80
cag caa cag cag caa cag cag cag cag cag cag cag cga cag cag cag      346
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Arg Gln Gln Gln
      85                  90                  95
cgg cag cga cag cag cag agg cag cga cag cag gag ccc tcc tgg ccc      394
Arg Gln Arg Gln Gln Gln Arg Gln Arg Gln Gln Glu Pro Ser Trp Pro
100                 105                 110                 115
gcg ctc ctg gcc agc atg ggg gag tcc tcg ccc gcc gcc cag gca cac      442
Ala Leu Leu Ala Ser Met Gly Glu Ser Ser Pro Ala Ala Gln Ala His
                  120                 125                 130
aga ctc ctc tcc gcc tcc tcg tcc ccc acc ctg ccc ccc tcc ccg gga      490
Arg Leu Leu Ser Ala Ser Ser Ser Pro Thr Leu Pro Pro Ser Pro Gly
              135                 140                 145
ggc ggc ggc ggc agc aag ggc aac cga ggc aag aac aac cgg agc agg      538
Gly Gly Gly Gly Ser Lys Gly Asn Arg Gly Lys Asn Asn Arg Ser Arg
              150                 155                 160
gct ctt ttt cta gga aac tct gcc aag ccg gtg tgg cgc cta gag act      586
Ala Leu Phe Leu Gly Asn Ser Ala Lys Pro Val Trp Arg Leu Glu Thr
              165                 170                 175
tgt tac ccc cag ggc gcc tcc tcc ggc cag tgc ttc acc gtg gag agc      634
Cys Tyr Pro Gln Gly Ala Ser Ser Gly Gln Cys Phe Thr Val Glu Ser
180                 185                 190                 195
gcg gac gct gtg tgc gcc agg aac tgg agt cgg ggg gcg gcc gcg ggg      682
Ala Asp Ala Val Cys Ala Arg Asn Trp Ser Arg Gly Ala Ala Ala Gly
                  200                 205                 210
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29

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tcg gat ttt tac ctt tca ttt tgt aat tcc tac aca ctt tgg gag ttg        778
Ser Asp Phe Tyr Leu Ser Phe Cys Asn Ser Tyr Thr Leu Trp Glu Leu
            230                 235                 240
ttt tcg ggg ctg tcc agc ccc agt act ttg aac tgc agt ctg gac gtg        826
Phe Ser Gly Leu Ser Ser Pro Ser Thr Leu Asn Cys Ser Leu Asp Val
            245                 250                 255
gtg ctc acg gag ggc ggt gag atg acc acg tgt aga cag tgc atc gag        874
Val Leu Thr Glu Gly Gly Glu Met Thr Thr Cys Arg Gln Cys Ile Glu
260                 265                 270                 275
gct tac cag gac tac gac cac cac gct cag gag aag tac gaa gag ttt        922
Ala Tyr Gln Asp Tyr Asp His His Ala Gln Glu Lys Tyr Glu Glu Phe
                280                 285                 290
gaa agc gtg ctg cat aag tac tta cag tcg gat gag tac tcg gtg aag        970
Glu Ser Val Leu His Lys Tyr Leu Gln Ser Asp Glu Tyr Ser Val Lys
            295                 300                 305
tcc tgt cct gag gac tgc aag att gtc tac aaa gcc tgg ctc tgc tcc       1018
Ser Cys Pro Glu Asp Cys Lys Ile Val Tyr Lys Ala Trp Leu Cys Ser
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Gln Tyr Phe Glu Val Thr Gln Phe Asn Cys Arg Lys Thr Ile Pro Cys
            325                 330                 335
aag caa tat tgc ttg gag gtg cag aca agg tgt cca ttc ata ttg ccc       1114
Lys Gln Tyr Cys Leu Glu Val Gln Thr Arg Cys Pro Phe Ile Leu Pro
340                 345                 350                 355
gac aat gac gaa gtc att tac gga ggc ctc tcc agc ttc atc tgc aca       1162
Asp Asn Asp Glu Val Ile Tyr Gly Gly Leu Ser Ser Phe Ile Cys Thr
                360                 365                 370
ggg ctc tac gaa acc ttc cta acc aat gat gaa ccc gaa tgc tgt gac       1210
Gly Leu Tyr Glu Thr Phe Leu Thr Asn Asp Glu Pro Glu Cys Cys Asp
            375                 380                 385
atc agg agc gag gag caa acc gca ccc aga ccc aaa gga acc gtg gac       1258
Ile Arg Ser Glu Glu Gln Thr Ala Pro Arg Pro Lys Gly Thr Val Asp
            390                 395                 400
aga aga gac tcc tgt ccc agg aca tcg ctc aca gtg tcc tcg gcc act       1306
Arg Arg Asp Ser Cys Pro Arg Thr Ser Leu Thr Val Ser Ser Ala Thr
405                 410                 415
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Arg Leu Cys Pro Gly Arg Leu Lys Leu Cys Val Leu Val Leu Ile Leu
420                 425                 430                 435
ctc cac aca gtg ctc acg gcc tcc gca gcg cag aac tcc acg gga ctg       1402
Leu His Thr Val Leu Thr Ala Ser Ala Ala Gln Asn Ser Thr Gly Leu
                440                 445                 450
ggc ctg ggt ggc ctc ccc acg ctc gag gac aac tcc acc cgg gag gac       1450
Gly Leu Gly Gly Leu Pro Thr Leu Glu Asp Asn Ser Thr Arg Glu Asp
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tga gcgcagccag gcgcgtgcgc agagcgcagg gctgggcagg gacacgcgct            1503
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actcagtttc tcacaccatt ttatacactg tgttttaacg tttggaggtt ttctttgctt     1743
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30

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<211> 467
<212> PRT
<213> mus musculus

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Glu Arg Ala Gln Lys Trp Arg Leu Ser Leu Ala Ser Leu Leu Phe Phe
        35   40   45
Thr Val Leu Leu Ser Asp His Leu Trp Phe Cys Ala Glu Ala Lys Leu
    50   55   60
Thr Arg Thr Arg Asp Lys Glu His His Gln Gln Gln Gln Gln Gln Gln
65   70   75   80
Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Gln Arg
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Gln Gln Gln Arg Gln Arg Gln Gln Gln Arg Gln Arg Gln Gln Glu Pro
            100   105   110
Ser Trp Pro Ala Leu Leu Ala Ser Met Gly Glu Ser Ser Pro Ala Ala
        115   120   125
Gln Ala His Arg Leu Leu Ser Ala Ser Ser Ser Pro Thr Leu Pro Pro
    130   135   140
Ser Pro Gly Gly Gly Gly Gly Ser Lys Gly Asn Arg Gly Lys Asn Asn
145   150   155   160
Arg Ser Arg Ala Leu Phe Leu Gly Asn Ser Ala Lys Pro Val Trp Arg
            165   170   175
Leu Glu Thr Cys Tyr Pro Gln Gly Ala Ser Ser Gly Gln Cys Phe Thr
            180   185   190
Val Glu Ser Ala Asp Ala Val Cys Ala Arg Asn Trp Ser Arg Gly Ala
            195   200   205
Ala Ala Gly Glu Glu Gln Ser Ser Arg Gly Ser Arg Pro Thr Pro Leu
    210   215   220
Trp Asn Leu Ser Asp Phe Tyr Leu Ser Phe Cys Asn Ser Tyr Thr Leu
225   230   235   240
Trp Glu Leu Phe Ser Gly Leu Ser Ser Pro Ser Thr Leu Asn Cys Ser
            245   250   255
Leu Asp Val Val Leu Thr Glu Gly Gly Glu Met Thr Thr Cys Arg Gln
            260   265   270
Cys Ile Glu Ala Tyr Gln Asp Tyr Asp His His Ala Gln Glu Lys Tyr
        275   280   285
Glu Glu Phe Glu Ser Val Leu His Lys Tyr Leu Gln Ser Asp Glu Tyr
    290   295   300
Ser Val Lys Ser Cys Pro Glu Asp Cys Lys Ile Val Tyr Lys Ala Trp
305   310   315   320
Leu Cys Ser Gln Tyr Phe Glu Val Thr Gln Phe Asn Cys Arg Lys Thr
            325   330   335
Ile Pro Cys Lys Gln Tyr Cys Leu Glu Val Gln Thr Arg Cys Pro Phe
            340   345   350
Ile Leu Pro Asp Asn Asp Glu Val Ile Tyr Gly Gly Leu Ser Ser Phe
            355   360   365

31

```
Ile Cys Thr Gly Leu Tyr Glu Thr Phe Leu Thr Asn Asp Glu Pro Glu
    370                 375                 380
Cys Cys Asp Ile Arg Ser Glu Glu Gln Thr Ala Pro Arg Pro Lys Gly
385                 390                 395                 400
Thr Val Asp Arg Arg Asp Ser Cys Pro Arg Thr Ser Leu Thr Val Ser
                405                 410                 415
Ser Ala Thr Arg Leu Cys Pro Gly Arg Leu Lys Leu Cys Val Leu Val
            420                 425                 430
Leu Ile Leu Leu His Thr Val Leu Thr Ala Ser Ala Ala Gln Asn Ser
        435                 440                 445
Thr Gly Leu Gly Leu Gly Gly Leu Pro Thr Leu Glu Asp Asn Ser Thr
    450                 455                 460
Arg Glu Asp
465


<210> 8
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide g713LF1

<400> 8
cgcttgcttc tgtctgtgta acc                                        23


<210> 9
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide g713LR1

<400> 9
gtatttgcgc agaccatttt aagatt                                     26


<210> 10
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide 713.LF1.5.1

<400> 10
actgtctgat tccacctatt atggag                                     26


<210> 11
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
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<223> oligonucleotide g713.LF1.5.1n

<400> 11
tgattccacc tattatggag agcac   25

<210> 12
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide g713RACE5R1

<400> 12
gggtagaagg gagacttagg   20

<210> 13
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide g713RACE5R-49

<400> 13
gggcatagca atcattc   17

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide g713CTGLF132

<400> 14
ggctgtgcgt tcccaaaata   20

<210> 15
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide g713RACE3N

<400> 15
aaaaatgttt cgttccagtc tgttaaga   28

<210> 16
<211> 29
<212> DNA
<213> Artificial Sequence

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<220>
<223> oligonucleotide g713RACE3Nn

<400> 16
attgctagaa ttgtttagca gtacatgca                                      29

<210> 17
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide SG1polyA

<400> 17
tttttttttt tttgacagag                                                20

<210> 18
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide SG1LR100

<400> 18
tttgccattt agcttagcag tacca                                          25

<210> 19
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide g713.PU

<400> 19
aatattctta acagactgga ac                                             22

<210> 20
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide g713.RP

<400> 20
ctttatagct atgaaatttc cc                                             22

<210> 21
<211> 24
<212> DNA
<213> Artificial Sequence
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<220>
<223> oligonucleotide g34301.PU

<400> 21
ctgatcactt gtggttctgc gccg                                    24


<210> 22
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide g34301.RP

<400> 22
aggactcccc catgctcgcc ag                                      22


<210> 23
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide SG1LR1102

<400> 23
aaaatactgg gaacagagcc agg                                     23


<210> 24
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide SG1LF790

<400> 24
gcacttagag cgcggggt                                           18


<210> 25
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide SG1LF834

<400> 25
gccggaggca gccca                                              15


<210> 26
<211> 17
<212> DNA
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<213> Artificial Sequence

<220>
<223> oligonucleotide moCTGR1511

<400> 26
tgtcctcgag cgtgggg   17

<210> 27
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide moCTGLR20

<400> 27
cggaggaggg gatacggaaa ttaaacc   27

<210> 28
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide moCTG1440

<400> 28
tgggtcactg ctgctctgtg ccaag   25

<210> 29
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> oligonucleotide moCTG5RACE1

<400> 29
tcacagtgtc ctcggccact   20

<210> 30
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
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<400> 30
tcctccacac agtgctcacg   20

<210> 31
<211> 983

36

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<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> 14
<223> n=a, g, c or t

<400> 31
aaaaaaaaaa aaanaacaaa aacaaaacat gaaacaggaa gacaggaaag atccatttga      60
cagagtactt gacacaggag agagaagaaa tactcatgta tctgaaagta ttcaaagggg     120
gagtgttagg agatgaatta atttaaaaaa tgagtaagag taaaatagtt taaagttaga     180
ccctgaggaa ctccagggaa gacaaagtaa cacaaggaac aagcaatgtt agccactgcc     240
taactttcct cagggtcatg tgtgcctcgc cataattatg taaacactta cattgttaaa     300
acgaaattcg gagaactagt ttgagtaaag gggaaaagaa agtatgttat tcatgtcgga     360
gttggaaata tgtgataggt tgaaattctc aatttcctaa ttggaaatca ttaagtcata     420
ctgaaacctg aaaattcaag aactgacaac acaattgatg ttgagatatg gaatttggta     480
cctgatgaaa gattagaaaa ttattaaaag caatttcttc tgggtggtgc tacaagatgg     540
aagaagaaag gacagaaagc tcttcataat caggtagacg ctttgacttt ttaagtggta     600
tgcctatatg cctttaaaaa acaactcaat ttaaaagaaa attaagagat gctaacagcc     660
gatttaaaga aaatttagta aaatattcaa ttgtataaag atacacaaaa tattggttat     720
ctacatgata gcaaagatga attaagggat ggggataaaa ctcttctcaa taacaccaaa     780
attaaaataa aacataattc atatatttag aaatatcatt acagaaatat gttgaacttg     840
tattaacagc ctctcctcaa aggtagcatg gagaatcatg caaacttaat ttggagatac     900
aaaaaaaatt gagaatgtgt agtgttgttc tttaattcta actgtaatgg ctgaataata     960
ttttgatcat gattgtgata cta                                            983

<210> 32
<211> 450
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 298
<223> 99-15663-298 : polymorphic base C or T

<220>
<221> misc_binding
<222> 275..321
<223> 99-15663-298.probe

<220>
<221> primer_bind
<222> 279..297
<223> 99-15663-298.mis

<220>
<221> primer_bind
<222> 299..317
<223> 99-15663-298.mis complement

<220>
<221> primer_bind
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<222> 1..18
<223> 99-15663.pu

<220>
<221> primer_bind
<222> 430..450
<223> 99-15663.rp complement

<400> 32
tcccaccttc ttctaaacgt gttgcttcaa tacgttgata ggtgaggaca cttaaaaatt   60
agactttata gaaataggtt ttttttttgtt tacatatata gttctttttgg tatcatatat   120
ttagcctctt tctaaaattt attttttgat actgaaggga gaaataggga gttattaatc   180
aacaggcatt aatttttagtc aagcaaaata aataagctgt agcgatctgc tctgtaacat   240
tgtacctaca gccaacaatt atatgttgtc cacttaaaaa tgtgttagat ctcatagyaa   300
ctcttcttac cacaataaag taaaaattct gaaacaataa gtgaatacct aaataataca   360
aacaaataca atattgtagt tttgggcact taataaatga cagcctcatt tctcaattag   420
agatcatcac aagttagaca gatgacgatg   450

<210> 33
<211> 476
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 398
<223> 99-15665-398 : polymorphic base A or G

<220>
<221> misc_binding
<222> 375..421
<223> 99-15665-398.probe

<220>
<221> primer_bind
<222> 379..397
<223> 99-15665-398.mis

<220>
<221> primer_bind
<222> 399..417
<223> 99-15665-398.mis complement

<220>
<221> primer_bind
<222> 1..20
<223> 99-15665.pu

<220>
<221> primer_bind
<222> 458..476
<223> 99-15665.rp complement

<400> 33

38

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cgtaaatgtg aaaagcatag cctcttcttg gaatgttaag tataaatatc tgaaatactg     60
ggcttgatat gtcaacagga gattgatgga taaaaataga attttatata aaaaacaact    120
ggacatatta gattgttaac ttggaagaaa gaccatattc aaagaagaaa acatagtgac    180
taatttcaaa catttaaagt cttccctgtg gaaacaaagg aatatctttg ttctaacact    240
tcaaagaaca gggttaaaaa atagactcac cacagagtaa atgcacaatt gacaatcgtg    300
aatgaattaa aaaccaaaca aaatattttg tcagctttct atctatgaaa ctaagaaaca    360
ggcttcctac taaggtaatg aatgtaattc acagagarca ttcacgtata agtttcattc    420
atgtttcaaa tttcattgat ttgatcaatg ggttattcta ataccctccc ttattt       476


<210> 34
<211> 547
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 166
<223> 99-15672-166 : polymorphic base C or T

<220>
<221> misc_binding
<222> 143..189
<223> 99-15672-166.probe

<220>
<221> primer_bind
<222> 147..165
<223> 99-15672-166.mis

<220>
<221> primer_bind
<222> 167..185
<223> 99-15672-166.mis complement

<220>
<221> primer_bind
<222> 1..18
<223> 99-15672.pu

<220>
<221> primer_bind
<222> 533..551
<223> 99-15672.rp complement

<400> 34
ccaataccat aactcctcta taggacatgg aagagtatta tatatgacaa atgattgcta     60
tgattattat tatcagtgtt attattatcc taatcctaag taatccaata aaagaaaaat    120
acatctgtgc ctgtgcgtat gtgcacgtgt gtgcagtcaa atacaygttg agtaaaggta    180
aagtctagct gtatttaatc aacctacctg aatcctcagg aaaaaattct aaacctagtt    240
taaaacatgt aaactctaag ctctctcctt atagtcagtt agtagcagca catcttaaaa    300
tctggtgtga atattctctt agttctacat gagtctaact aaacagagga ttattcttag    360
gtgtttgaaa gagacatatg tgacactgct gttttgagaa caatttaagt gttgtcttgt    420
catgtacaga agttctcata ttactttaca taaatggttg cataattgtt ttatagtaaa    480
taatagactg tcaatatttc taggataact ccaaaacaaa atttcctaga mmacattttg    540
```

39

aaaaggg   547

<210> 35
<211> 502
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 185
<223> 99-15664-185 : polymorphic base G or T

<220>
<221> misc_binding
<222> 162..208
<223> 99-15664-185.probe

<220>
<221> primer_bind
<222> 166..184
<223> 99-15664-185.mis

<220>
<221> primer_bind
<222> 186..204
<223> 99-15664-185.mis complement

<220>
<221> primer_bind
<222> 1..19
<223> 99-15664.pu

<220>
<221> primer_bind
<222> 483..502
<223> 99-15664.rp complement

<220>
<221> misc_feature
<222> 54
<223> n=a, g, c or t

<400> 35
gtttaccatt agcactgtca tatttgtgtg acttgtcatt ctctacagcg gagnacgggc   60
tggcacgggg cctgatgctg acttgcacaa gggaagcctc ctgtctctga cttccccagg   120
ataattcctg gggaaagtgt gctccctagt gttaagagcg gtttaatggc tggagggttt   180
cagckggctg accaggcaga gaaggagggt gaatcacctc tcagcactct ccacttagac   240
tttgtgtggt cgtcgggtgg tcaaaccttc taactagttg tattgcagat ttggcattcc   300
agtgcaaaca aaagacagaa acacaatgtt cacatgcttt ccagagatca cctggatatc   360
agatcatttg attttcaagt aagtcgaaac cttggtggaa atcattaact atcctgttta   420
tgaccaaaaa ataaaatccc aaatttcttc tcttcatttc ttacctgctt taaaattgta   480
tccaaagcgt graagtaaaa ga   502

<210> 36

<211> 455
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 205
<223> 99-5919-215 : polymorphic base A or G

<220>
<221> misc_binding
<222> 182..228
<223> 99-5919-215.probe

<220>
<221> primer_bind
<222> 186..204
<223> 99-5919-215.mis

<220>
<221> primer_bind
<222> 206..224
<223> 99-5919-215.mis complement

<220>
<221> primer_bind
<222> 1..19
<223> 99-5919.pu

<220>
<221> primer_bind
<222> 435..455
<223> 99-5919.rp complement

<400> 36
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ctacagcaat gcagatttca attctgccat tgaattccca gacatattcg tcatccccat      60
tttcatcccc caccaccctg ccattttctt cgtgttaact tgtttttcctg actcacagaa    120
atcacctttt cctgtataca tttttaggat gtcagacttt attctaatga tttctcctag    180
ttgcccccca aaattgtatt ctacrgtgtg attttaaagc tgaattttca agatgatatt    240
tcatatctat attttcacaa gcttttcttc tatgaatgtt attgtcagct gtcagggtgt    300
gagatggtac ttgatactac attctttcca agctgttgcc tgaatcggtt taagacaaag    360
tcattactag gctgtaaact gttgctctgc aaaattgagc agcacgtatt taaccactca    420
tacttcttag ctctccaaca ctttgagtca ataga                               455
```

<210> 37
<211> 450
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 157
<223> 99-5862-167 : polymorphic base C or T

<220>
<221> misc_binding
<222> 134..180
<223> 99-5862-167.probe

<220>
<221> primer_bind
<222> 138..156
<223> 99-5862-167.mis

<220>
<221> primer_bind
<222> 158..176
<223> 99-5862-167.mis complement

<220>
<221> primer_bind
<222> 1..20
<223> 99-5862.pu

<220>
<221> primer_bind
<222> 430..450
<223> 99-5862.rp complement

<400> 37
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aatcaaggta gagatgtatg agaaatagcc ggttaaagaa acagcattac tttcagacta      60
tcttttattt gaaatacacg tggggaaacc agaaggtgaa accccttagg agatggatat     120
aggatactaa aatctgagtt agaaaaattt gagcatyagc accttacgtg tcatgctaag     180
atagtgaatg agactgcaca ggaattgcat gcagtttaac ggaaaaagaa gtcgaaagat     240
aaattcctag aacactaaca ccgagttatg ggaggagaaa tatcctgcac aggtcactct     300
gggagacatg tcaattgttt agccaatatc catttaactc atctttcttc ctaatgaaaa     360
ccgaatttgg agaagcaggt agtgcccctg gctagaaata tgaaccttcc cagcttctct     420
catgcactga actgacaaag ttcaggtctg                                      450
```

<210> 38
<211> 403
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 292
<223> 99-16032-292 : polymorphic base A or C

<220>
<221> misc_binding
<222> 269..315
<223> 99-16032-292.probe

<220>
<221> primer_bind
<222> 273..291
<223> 99-16032-292.mis

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<220>
<221> primer_bind
<222> 293..311
<223> 99-16032-292.mis complement

<220>
<221> primer_bind
<222> 1..19
<223> 99-16032.pu

<220>
<221> primer_bind
<222> 384..403
<223> 99-16032.rp complement

<400> 38
gttgttaccc cacttcttcc ccccagctcc cccttcctca cacagttcat gccacatgcc      60
actctcctgg actactggaa atgcgtcagt ccactctggg ctcatcccat catcccccat     120
gctgcaacct gagagagagt tgcaagttgc aaatctgatc ttgtcaccac cactctccac     180
actaaatccc tctaatgcct cccccttct ttttggataa attccttctg cttgcatagc      240
cacgtggttg gcttctatag catcacttca cactgtggtc acctgccttc tmctcactca     300
ggaacttctc tccattgaag aagttcttct tccccatctc cagggctttc ccactgacag     360
ttgtatctcc cccataccaa gcccaggtgg tcatctcatc cca                       403

<210> 39
<211> 476
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 118
<223> 99-16038-118 : polymorphic base A or G

<220>
<221> misc_binding
<222> 95..141
<223> 99-16038-118.probe

<220>
<221> primer_bind
<222> 99..117
<223> 99-16038-118.mis

<220>
<221> primer_bind
<222> 119..137
<223> 99-16038-118.mis complement

<220>
<221> primer_bind
<222> 1..19
<223> 99-16038.pu
```

<220>
<221> primer_bind
<222> 456..476
<223> 99-16038.rp complement

<400> 39
gttgcttatt ctttctctct tctgcagggt ataaaggaat ctgaacacga ctgatatttt   60
ctttaatttt tagatccaga tatacattgg gtaaaatcta cttcataggt tttcaaarga   120
gcattcttct gagcaaatct gaaaactctc taaactctat tggtatgtta ctctttatct   180
ttatatgaat ttaaattctt ctagaagtta gataaaactg tggtaaagct acataatact   240
tttgacatat tttcaagcgt agacaaactt caattaattt gtaagataca ggaagaaaat   300
ttttccagtt aaaatgtacc tcttggtttc tggagtgtta gcaaccattc acacttacag   360
ttcaaacagt gcaaccttgt aaaacatata taacttatga agagatcgat atctcttttt   420
ataaagcaaa caagtaaatt tttccctcaa tccatgattt atttttgtga agtggg   476

<210> 40
<211> 498
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 133
<223> 99-5897-143 : polymorphic base A or C

<220>
<221> misc_binding
<222> 110..156
<223> 99-5897-143.probe

<220>
<221> primer_bind
<222> 114..132
<223> 99-5897-143.mis

<220>
<221> primer_bind
<222> 134..152
<223> 99-5897-143.mis complement

<220>
<221> primer_bind
<222> 1..18
<223> 99-5897.pu

<220>
<221> primer_bind
<222> 475..492
<223> 99-5897.rp complement

<400> 40
aaaagtgttt gccagtcctg tttcttacag agcacagaac tcagatgctc ttataaagat   60
acaggataaa tcacatcatt tcctgctcca tcatcagaat attattatat gatttagatc   120

44

```
acttttttaa aamagaacat ggacttagta cagaacaaca gcaaaagcct ggggaaggag      180
aggagtgcac catgaggagt caatggggag cagaagccag tccatttgac tgatttggtt      240
cgtgtgcaaa ataattgcta aataattgca tatatgtgag actccgggta ttttcaaaac      300
cagctggcaa aattgtgtta ttctctaccc tctgctggct ttcacgggtt ctctgttctc      360
tctccttttc ctccattctc ctcttaccct aattcctgac cactgtaatc caataatcta      420
aggttttagg atttggatga ctaaggttac ccatggaatt gtttggaaat gtagacctgt      480
aatggagagg ggagaaaa                                                    498
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<210> 41
<211> 517
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 360
<223> 99-13601-360 : polymorphic base A or G

<220>
<221> misc_binding
<222> 337..383
<223> 99-13601-360.probe

<220>
<221> primer_bind
<222> 341..359
<223> 99-13601-360.mis

<220>
<221> primer_bind
<222> 361..379
<223> 99-13601-360.mis complement

<220>
<221> primer_bind
<222> 1..19
<223> 99-13601.pu

<220>
<221> primer_bind
<222> 500..517
<223> 99-13601.rp complement

<400> 41
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gttttacttg acagttacca agaattgttt cgcatttaag aaaattatat ctttgatggt       60
tccctcatta atggtgcctg gatacccaat gcaacacacc tacatcaaac tgcatttgta      120
actgttggat tcataatgat tctacctaag atgcaagcat acggcatcat tgtgccttgt      180
tgtatggata tgcttgagaa gtcacatgct gaaatacata tattttaaat ttgacagtat      240
ctcctacaat attttcttta tattatagta aggtattaca ttacagttta aaacttatga      300
ctataagcag gtgatattat ctatgaattt catgtgaaat tagcaaaggg acagtctcar      360
atgtttgctg tataaagtgt atttgaagcc tgatagggtt gagaaacact cagctacagt      420
aagtaaaaac agctctctta gtggttgcct tgttgagaag atcttgaaaa caaggttgaa      480
aatacaaaag aaactgtgtg gagtctacaa agatatt                              517
```

45

<210> 42
<211> 533
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 97
<223> 99-13925-97 : polymorphic base A or G

<220>
<221> misc_binding
<222> 74..120
<223> 99-13925-97.probe

<220>
<221> primer_bind
<222> 78..96
<223> 99-13925-97.mis

<220>
<221> primer_bind
<222> 98..116
<223> 99-13925-97.mis complement

<220>
<221> primer_bind
<222> 1..20
<223> 99-13925.pu

<220>
<221> primer_bind
<222> 513..533
<223> 99-13925.rp complement

<400> 42
catggaagta aaagcatatc ttcattataa gacttctaca caaattatca catctttact   60
tacagcagct gaaacctgga aacaactcta atgcccrtca acagaggaat ggatggataa   120
agaaactgtg atgcagtgga atacgactca acgaagatga gactaaaaat aattatactg   180
agtaaaagaa tccaaacaaa atagagcaaa cactgtgcca tcctgtttat accttactcc   240
agtaaatgca aactaataca caatgaaaaa aattacttat ttgagaactg gggagaggaa   300
ggagagggaa aggggtagat aaagaaaaga ggagagatta aaaggagcat aagaaaacct   360
cagagaataa taggtttgtg gtaaacatta ccgtggtaat gtttttaggg tatattcaca   420
tgtaaaaact tatccaatta tacattttaa atatgtacag tttagtgtgt cagttatgcc   480
tctgtaaagt tgattttaaa aaaagtccta ttccaagtym acaatttcat ttg   533

<210> 43
<211> 480
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 201

<220>
<221> misc_binding
<222> 178..224
<223> 99-13929-201.probe

<220>
<221> primer_bind
<222> 182..200
<223> 99-13929-201.mis

<220>
<221> primer_bind
<222> 202..220
<223> 99-13929-201.mis complement

<220>
<221> primer_bind
<222> 1..19
<223> 99-13929.pu

<220>
<221> primer_bind
<222> 460..480
<223> 99-13929.rp complement

<400> 43
```
gggagaatac taataatgga agcattactt ttattttttc tataaattcc tctggaaata    60
tgtatttctt atgtcctaag gttattaaca aaaagagaaa ataatttctg atttataatt   120
cactttcctt caaaaaataa taactcagtg tctagtaagg taaagcaaaa aaagttaaaa   180
gaacccataa gtttatttta maatacctac tcagaagcaa aactgacttt ctattaaaaa   240
ttaaaaaaaa aagttttctt attattgttt tgtttccttg ttttttaggtg atgggattgt   300
atttgcaact ctctggtcag taagtgataa aatgccattt ctatgcaccc acctggcctg   360
tgtgactggg agaatctctc tttttattaa atgtgcttca agttttaaca actgactttt   420
gttagtgata tgatttatct acccgtgact gtcaaacaac acagatgatt tgcatatctc   480
```

<210> 44
<211> 477
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 108
<223> 99-14021-108 : polymorphic base A or G

<220>
<221> misc_binding
<222> 85..131
<223> 99-14021-108.probe

<220>
<221> primer_bind

<222> 89..107
<223> 99-14021-108.mis

<220>
<221> primer_bind
<222> 109..127
<223> 99-14021-108.mis complement

<220>
<221> primer_bind
<222> 1..18
<223> 99-14021.pu

<220>
<221> primer_bind
<222> 460..477
<223> 99-14021.rp complement

<400> 44
```
tttgttgtta atcgcccctt ttctgcaaca cttgtgggtt agggaaaata attctaaagc    60
aagagcaaag acagagttgg gagatcacca gtgaggttca attttccrtc acattcactc   120
tgctccacac ctcagataat catgtgctta actgcgaaac ttgcttgaca attacagaac   180
actttctcac ccattactac cttgatcctc acaattctgt ggggtagtag gagcagatgc   240
tgaaattgcc atacgcaaat cagtgaactg aagcttagag acctccagca ggggcagagg   300
gtcagcggaa actatcccag ggttcagcca acaagaaagt atattggaat cagagtatta   360
aaataagaat aataaaacca actaaaattt accgtgcttt ttatttccac tcagtgccaa   420
caattcttaa cagtgtcagt gatggatccc tgtgccccag gggacagact tcttact      477
```

<210> 45
<211> 475
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 314
<223> 99-14359-314 : polymorphic base G or C

<220>
<221> misc_binding
<222> 291..337
<223> 99-14359-314.probe

<220>
<221> primer_bind
<222> 295..313
<223> 99-14359-314.mis

<220>
<221> primer_bind
<222> 315..333
<223> 99-14359-314.mis complement

<220>

```
<221> primer_bind
<222> 1..18
<223> 99-14359.pu

<220>
<221> primer_bind
<222> 457..475
<223> 99-14359.rp complement

<400> 45
ataagggaat ggtgtgaggt gggaccagag gaggctgcac tgagaaagtg agaggggcaa      60
gacctcaggg gaagaaggga gggctgcacg gatgtctcag gcagagcagg cagcaccgga     120
aaaggtgggg gacactcctt ttggaccagc atataatttg gttaaagcct ctcctgtttc     180
acctaatata taagcacatt tcaagataaa actactactt tattgtcatc aaatataaaa     240
gtaatttttt attcagggtt ttctaatact catctataaa ggcatttctt tcccacatgg     300
catgtgttac aggstgttta acttaaagca attgtaaaag aaaagcctga agaaataagt     360
ctacaacgat ttacatcgtg tttatttttg tgtcaaaata tatgttaaaa tatacattag     420
ctatactaag ggaatcaaga gaagatcata attgctctta tgacttggga tttag          475
```

B'
con

```
<210> 46
<211> 473
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 316
<223> 99-14364-415 : polymorphic base C or T

<220>
<221> misc_binding
<222> 293..339
<223> 99-14364-415.probe

<220>
<221> primer_bind
<222> 297..315
<223> 99-14364-415.mis

<220>
<221> primer_bind
<222> 317..335
<223> 99-14364-415.mis complement

<220>
<221> primer_bind
<222> 1..19
<223> 99-14364.pu

<220>
<221> primer_bind
<222> 453..473
<223> 99-14364.rp complement
```

<400> 46
```
gtgttttaat tcaacccagc tataagatac gaaatgatag aattgctcta gattctctat      60
tggttaaata aggagatatt tgtgctattg ccaataatac atgctgtacc tggataaacc     120
cctttgggca agttgtgatg caaatactca agaaaatagg ccacatagtt acaacaggac     180
ttacctaatt ccccatggtc atttggctga ttcagtcagt tgctttcaag cctaggttct     240
tggctcaata ttattacata aactagaatt ttcctattac tattaatttt actttgtatt     300
tttctttata aacttygtac ttattgcttg tcaaatttca gcagaagtac aactcctgag     360
agaataatgc tggctcagag ttttgagatg ataacccttg tctatgaaac tgatgaagtt     420
ggacttaaca acgaacactc cccacagaac tcctgatgct caaatgtggc taa            473
```

<210> 47
<211> 502
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 99
<223> 99-15056-99 : polymorphic base C or T

<220>
<221> misc_binding
<222> 76..122
<223> 99-15056-99.probe

<220>
<221> primer_bind
<222> 80..98
<223> 99-15056-99.mis

<220>
<221> primer_bind
<222> 100..118
<223> 99-15056-99.mis complement

<220>
<221> primer_bind
<222> 1..18
<223> 99-15056.pu

<220>
<221> primer_bind
<222> 482..502
<223> 99-15056.rp complement

<400> 47
```
caggaaactc acaagaagsc agatttcctt cgagcacctc ctgaataaag aggcaaaggc      60
cttcttaact cttacaattt acaagtggct atgagtgcyt ttatagttcc cataataatt     120
tctccacgta gacttcctaa ataataattt ctcctgtttt atattctctg tgcttatgtt     180
tatatcaaac aagttaccac ttaatcaaat gccgatttgc attgctcact atgtaacttt     240
aattttcttt gcctcttatt tttggatctt aattctaaaa ctagatgatc ataaattcat     300
ttaggaataa gcttgtgatc tagccttctt ttgaacccct ttgtgctcct cacaatattt     360
gtttcgatga aacagtgagc aacatttgat ctatgattgt taatagaaaa acaccaatgt     420
ctcaagttat tgtaaacata ggcataattg acctttggtt ctataaatat gtttggtgtt     480
```

50

ccccaaaata cgtctccctt tt   502

<210> 48
<211> 494
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 412
<223> 99-15229-412 : polymorphic base A or G

<220>
<221> misc_binding
<222> 389..435
<223> 99-15229-412.probe

<220>
<221> primer_bind
<222> 393..411
<223> 99-15229-412.mis

<220>
<221> primer_bind
<222> 413..431
<223> 99-15229-412.mis complement

<220>
<221> primer_bind
<222> 1..20
<223> 99-15229.pu

<220>
<221> primer_bind
<222> 476..494
<223> 99-15229.rp complement

<400> 48
ctgtcattga gaaatgctac caataatact tagagaattt gatacaactc agtctgaaaa   60
agctaagatt agcagaacag agctgtctcc aaatatttga agaactattt tatttaaggg   120
attggaccca tttttgtatg tagttccaga ggagcagatg gtgaccactg tccaggcaga   180
tgtgtctcaa tgtaaggaca acatctgtaa tattaataat tagaatgtat cctgtaattt   240
tctctctacc cttggaaacc agtcgagatc cagagtcttt cactgggagg cttaaagcct   300
agagcagcct tggtgctaga ggcggacagg gataatgaac taatcttgaa ccaattcatc   360
catagcaatc tcaatgcttt cgttagctct tataggtatt taatacggcc avaggaatga   420
aggtagtctt gctggtttag aagccctgcc taccacaacc cctacaccac cccatcccct   480
gcatagtctg atgt   494

<210> 49
<211> 485
<212> DNA
<213> Homo sapiens

<220>

<center>51</center>

```
<221> allele
<222> 291
<223> 99-15232-291 : polymorphic base G or T

<220>
<221> misc_binding
<222> 268..314
<223> 99-15232-291.probe

<220>
<221> primer_bind
<222> 272..290
<223> 99-15232-291.mis

<220>
<221> primer_bind
<222> 292..310
<223> 99-15232-291.mis complement

<220>
<221> primer_bind
<222> 1..18
<223> 99-15232.pu

<220>
<221> primer_bind
<222> 467..485
<223> 99-15232.rp complement

<400> 49
caatagaaca ggctgctcct ttataattat taatcatagt gtatattaat tcatcatcac      60
atacgtggct agaaaaaaat ttagaacaaa aagatatgtg atatgtaaag gcctacgata     120
attcagactt ctttgaggag agcttttatt ttattgttat tcttatttta tctcttgtca     180
atataaattg agagaataaa cagacaaaca ttacaaatta gtgattaatt gcatttaaag     240
cctagttaag actatttaag actattatgc ataatacagg aaaactacct ktattatttta    300
tagtgggtgc cttctgaagg atctgaagga gaatcagttc tatgcctctc tcctcattcc     360
caggaggtgc ctggcattcc ttggcttgta gacgcatcac cctaatctct acctctgcct     420
tcacatggtg tcccctgtgt gtgtgttttt gccccatgtg tctcctcttt ttatatggat     480
gccag                                                               485
```

```
<210> 50
<211> 464
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 347
<223> 99-15241-347 : polymorphic base A or G

<220>
<221> misc_binding
<222> 324..370
<223> 99-15241-347.probe
```

52

<220>
<221> primer_bind
<222> 328..346
<223> 99-15241-347.mis

<220>
<221> primer_bind
<222> 348..366
<223> 99-15241-347.mis complement

<220>
<221> primer_bind
<222> 1..19
<223> 99-15241.pu

<220>
<221> primer_bind
<222> 444..464
<223> 99-15241.rp complement

<400> 50
gttatgggtt gaaaatctct gagttcttgt acatacaaaa attttactgt tgtcacagtt   60
gaatcttagt ttagatgggt ataggatttt tattcaaaat gcttttactc cataagttta   120
aaaatattgt tacattttcc tcaagtatct gatgttattg atgagaagtt taattctaat   180
ttgactcttg ttcccttgta ggtactattt gttttccagt ttgggaagct tacatttctt   240
aaaattcaca acatataatt tacatactac acaattcttt ttaaagtata caattcaatg   300
catttagtat gttttagtac atataactta aattatgtat atacaaratc tctttataat   360
atttgtagaa tatgtagcat attcacaaga ttgttcaacc atcaccactc tctatttcca   420
gaatcttttc ctccaaaaag aaaccctgaa cactatgatg aata   464

<210> 51
<211> 550
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 196
<223> 99-15244-196 : polymorphic base A or G

<220>
<221> misc_binding
<222> 173..219
<223> 99-15244-196.probe

<220>
<221> primer_bind
<222> 177..195
<223> 99-15244-196.mis

<220>
<221> primer_bind
<222> 197..215

53

<223> 99-15244-196.mis complement

<220>
<221> primer_bind
<222> 1..20
<223> 99-15244.pu

<220>
<221> primer_bind
<222> 532..550
<223> 99-15244.rp complement

<400> 51
ctgcttctgg ttatgttttc ctaattgcca aaatggtaaa aatgagaata atcattgaaa   60
gagaaagcat aaagtagcaa aaatcctttc cagattaaaa aacgaagcaa agcatgtttc   120
ccaagtaata atactctcat cttcctccct aatcctttac cccactacca gaagaagagt   180
aaaatgtccg gatatrtttg aaggtaaaga tttctccttt taataaaatt agtcaccttg   240
tacacatcag tagatcttga gaatgaaaag cttttctagt acattcattt caacctataa   300
atgtttgact tttctctgtc attcatttac gacctgtgat cttttcattc cctttcagtt   360
agaatatttt tcaaattttt attgatattt tctatttaac ccataggtta tttggaaata   420
cattgtttaa tttctaatat atttgctttt ttttctactt atttcttttt ttcttaattc   480
cacactggtc caaatatatt ctgcatatga tttaatattt taagttctgt agagactaac   540
cttgtgccct   550

<210> 52
<211> 452
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 404
<223> 99-15252-404 : polymorphic base C or T

<220>
<221> misc_binding
<222> 381..427
<223> 99-15252-404.probe

<220>
<221> primer_bind
<222> 385..403
<223> 99-15252-404.mis

<220>
<221> primer_bind
<222> 405..423
<223> 99-15252-404.mis complement

<220>
<221> primer_bind
<222> 1..18
<223> 99-15252.pu

```
<220>
<221> primer_bind
<222> 433..452
<223> 99-15252.rp complement

<400> 52
atggggggcat atagcaaccc tttagaaaca aaactacaaa aggtaagctt gtcttcttgc      60
atttcctttc tcttactaca tttaacatgg gaggttttct atgtctcaca ttcaaatatt     120
ctcactcggg ctgcctaatt tttccctgat tttccatcac tctttatgaa ggcttgctac     180
tttagaatac acattttctt aacagaagat aataatcaga agatgtctcc caaatataag     240
tccaaatctt tcctatcatg ctgtgttctt tggctctttt gactttattt gaagtcagcc     300
ttgaagggga tagagatagg ctgtatgaag tccacgctga gaagttttgc cctgccctac     360
ttgtcctgta atatttcatg gatagcccag tggtgattaa accygtgtgt acaggaataa     420
ccatgagaat ttgttaaaaa tataggctct gg                                    452


<210> 53
<211> 477
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 382
<223> 99-15253-382 : polymorphic base C or T

<220>
<221> misc_binding
<222> 359..405
<223> 99-15253-382.probe

<220>
<221> primer_bind
<222> 363..381
<223> 99-15253-382.mis

<220>
<221> primer_bind
<222> 383..401
<223> 99-15253-382.mis complement

<220>
<221> primer_bind
<222> 1..19
<223> 99-15253.pu

<220>
<221> primer_bind
<222> 459..477
<223> 99-15253.rp complement

<400> 53
aaaatcaatt ccccaacact cattttgtac gctaattttg taagatcctg aaaagtttca      60
ctattttatg gtttcatgtg ttacagatga aaaaaaaact agaattcaaa ttttctgagt     120
ttttttttac aatattttat gattacaaag ttagaagact aagaataaaa tggcctaatt     180
```

```
tccataatgt gagtggtaaa tgcagagcac tggcctaaag aaaatatttc aaaaaattag    240
tcatctttc cttaattttt ttccaaccta tgatctgttg aatgagcatt ttgcatatat    300
aaataaataa attactttgt aaataatctt gactggtttc tgttgaccac agtaacccac    360
tgcacagcac agcctgtaat tyctatgaac ctagggaaat gtatttaagt ttattttttg    420
attacacagg tcctcattgt gtaactaaac attgcataga atatgccagt gatgatg       477
```

<210> 54
<211> 456
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 392
<223> 99-15256-392 : polymorphic base C or T

<220>
<221> misc_binding
<222> 369..415
<223> 99-15256-392.probe

<220>
<221> primer_bind
<222> 373..391
<223> 99-15256-392.mis

<220>
<221> primer_bind
<222> 393..411
<223> 99-15256-392.mis complement

<220>
<221> primer_bind
<222> 1..18
<223> 99-15256.pu

<220>
<221> primer_bind
<222> 439..456
<223> 99-15256.rp complement

<400> 54
```
cctctctatg atgcttccta ttaagcaatt ggggaaatgt aataaacaag ggttggtgag     60
catcttcctt agtgagatgt ttttggaaga attggataat tgagtgaata atagtgagaa    120
actcctgtgt ctgatgttgc tccatgttgg aatgctttta tgttctcaga gaatgagtca    180
ctgagagcca attgtgatga tacacaatgg ttttacccag gttggatatg tcctctgta    240
ctggtaccct ttaagtcagt ggcactaatc agtcagtcat tgtcatgctt tgtgttggtc    300
catcatatgg tatgccctct tagagaacat cctgattagt ccttagacat cttttcaatt    360
tgaacactgg ggctcctcat tcgggtaaaa aytatggaca gtcagtgaaa ctgttgcaat    420
ggcccctcat agcagattgg atctcaatgc actttg                              456
```

<210> 55
<211> 501
<212> DNA

56

<213> Homo sapiens

<220>
<221> allele
<222> 200
<223> 99-15261-202 : polymorphic base A or G

<220>
<221> misc_binding
<222> 177..223
<223> 99-15261-202.probe

<220>
<221> primer_bind
<222> 181..199
<223> 99-15261-202.mis

<220>
<221> primer_bind
<222> 201..219
<223> 99-15261-202.mis complement

<220>
<221> primer_bind
<222> 1..19
<223> 99-15261.pu

<220>
<221> primer_bind
<222> 481..501
<223> 99-15261.rp complement

<400> 55
```
cttctaatcc tttgtttcca cttattttat ttcattcctc attttatccc tttttttctaa        60
attccatttt attatactta aggtgctttt aatatggtta tcatactcct gatagtgtta       120
tttctttctt agtcttctta tataagcgct atacgttcac attccatctc ctttggttat       180
ctttccattt cttcaccgar cctctttgct ctcttttttt atagctggtt cactcaaaat       240
gtcttacttt gccatttttg aaatttattt tcattctttt atgtactgaa taaaatttaa       300
aaatacttta tcatggtggg aggtacccgt gatgtccaaa taagtgttta tattaattgt       360
tggggttttt ttgtttgtgt gttttttgaa aggttaagaa aatctcattc agaaagtaag       420
ttgtttaaaa attctggacc aaatttacca cacatcaagc agatacttac caagttgttt       480
ggtagacatt agcagtattt a                                                 501
```

<210> 56
<211> 541
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 432
<223> 99-15280-432 : polymorphic base C or T

<220>

<221> misc_binding
<222> 409..455
<223> 99-15280-432.probe

<220>
<221> primer_bind
<222> 413..431
<223> 99-15280-432.mis

<220>
<221> primer_bind
<222> 433..451
<223> 99-15280-432.mis complement

<220>
<221> primer_bind
<222> 1..18
<223> 99-15280.pu

<220>
<221> primer_bind
<222> 521..541
<223> 99-15280.rp complement

<400> 56
atgtccatcc atcttgccca gagagagttt ctacaacact tcctctgcaa gccctttccc   60
tacttgcctc acctattgct ttcctctgtt acgttgtatt cccctcactg tttcttccaa   120
catcttccca cctcagagca tggacacttg ctgctctttc tgtgtcatga tgctgctcac   180
ttgtcccttt cttaatgtct cctccctgag ccaatcttct ccacccccac aacttacgca   240
cacttacatg tcatattttc cttcatagcc tttaacacca tttgaaatga tatatatttg   300
attgctttta aaatttctct gtccccccac taaatataaa cttcaggatg gcaagaatgt   360
agtccattat cttatttctc cagcctccat acttttaaga aaataaattt tggttgtata   420
agccatccag tyagtggtac ttggttatag cacccctagc aaaagaatac aaaaaaaggg   480
agaatgtttg caatcatctg tttgaggcta ggaattccca gagagggaaa caaggagtaa   540
t   541

<210> 57
<211> 514
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 428
<223> 99-15353-428 : polymorphic base C or T

<220>
<221> misc_binding
<222> 405..451
<223> 99-15353-428.probe

<220>
<221> primer_bind
<222> 409..427

58

<223> 99-15353-428.mis

<220>
<221> primer_bind
<222> 429..447
<223> 99-15353-428.mis complement

<220>
<221> primer_bind
<222> 1..18
<223> 99-15353.pu

<220>
<221> primer_bind
<222> 495..514
<223> 99-15353.rp complement

<400> 57
```
tgggaatgga ggtagtagac gatgaggtct ccaccctctg actttgcaga gatgggcaag      60
gccaagtgtt ggaagggctt aaacacacac cggagtattc tgtgagaacc agtggatttc     120
agaggatggc aatgacacca cttgccttct gcctcaggag gataactgat ggccgtgtgt     180
gggatgcact ggagagcaag agctggcttg cagggagacc agctggatga ttttctttca     240
tttattttat tcattcaaca cacattcatc tggggttcac tctgtgccca acactgggca     300
tttccaaata gtccagatgg cagtaagcat ggttgtggca gtaggaatgg gaaggctggg     360
aggggtatga gaggcattac aaacgggaag tgggagtggc accccagaaa agtctagttt     420
aaggtgcyag tggatgtgtg catgtgtgcg cggggggtgtc tagagggtgg cgggcagctg     480
gaaattgagg tcaagtgctt aaagaacaac tcgt                                  514
```

<210> 58
<211> 489
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 150
<223> 99-15355-150 : polymorphic base C or T

<220>
<221> misc_binding
<222> 127..173
<223> 99-15355-150.probe

<220>
<221> primer_bind
<222> 131..149
<223> 99-15355-150.mis

<220>
<221> primer_bind
<222> 151..169
<223> 99-15355-150.mis complement

<220>

<220>
<221> primer_bind
<222> 1..18
<223> 99-15355.pu

<220>
<221> primer_bind
<222> 471..489
<223> 99-15355.rp complement

<400> 58
taacttctcc gtctctcctt cttagcccat atgtcaataa tgactgaaag tattcatttc   60
catctttaaa ctgcctattc cagccacctc ccacctccat ctctttcctt ctaagttttc   120
ttcatcttct actttgggca aaaggaaaty gatgtgtcag acaggcctag ttttgaattc   180
tggatctgct agcacttctc tgtgtgtcct tggttatatg atatagtctt aaaccttaat   240
gttcttgcct gtaaaatggg gataataaaa acctcttaac agtggttgtt tcatgcagct   300
ttcattacaa acttcctcat tcaaaatctt caatgatttc catttttcac aaaatgaaat   360
tcaaaatttc tgtagattat tgagacaagt cccctactct tcacctaaat ttatctttta   420
tttattctct catcattatc aacaactact aggctttgtt gccttgactc cagaggcaaa   480
aatcttatc   489

<210> 59
<211> 468
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 227
<223> 99-15685-227 : polymorphic base A or G

<220>
<221> misc_binding
<222> 204..250
<223> 99-15685-227.probe

<220>
<221> primer_bind
<222> 208..226
<223> 99-15685-227.mis

<220>
<221> primer_bind
<222> 228..246
<223> 99-15685-227.mis complement

<220>
<221> primer_bind
<222> 1..18
<223> 99-15685.pu

<220>
<221> primer_bind
<222> 449..468
<223> 99-15685.rp complement

60

<400> 59

```
aaacaaaggc acgcagagga taaggcatga gtccaaccag cagcatctcc ctcccgaatg    60
agtacagaaa tgatcaatac tcgaagagaa aaagatgctt tcagtgtgct ttacctgaaa   120
acttccttaa gcagcttcac tttattgtca ggatatcgct ttgtgtttgt atcatctaag   180
aaagctcgcg catatgctag tgggccagca ttgacctaga caaagarcaa agattttcag   240
ttccactagg aagaaaatca ccatgaccat ctgctcagtt tcagtttgca ggcactaaaa   300
agcccgttcg cgtgagctac tcacaatccc tgccttccag gaacttaagc ccaaaaagaa   360
accacaaagc tcactctgtt gcacaccact tgattccatg atctcagcca tcttcagggc   420
acttgtgatg atggtttact ttatgtaaga agaaaccaat gcttggaa                468
```

<210> 60
<211> 500
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 428
<223> 99-15695-428 : polymorphic base C or T

<220>
<221> misc_binding
<222> 405..451
<223> 99-15695-428.probe

<220>
<221> primer_bind
<222> 409..427
<223> 99-15695-428.mis

<220>
<221> primer_bind
<222> 429..447
<223> 99-15695-428.mis complement

<220>
<221> primer_bind
<222> 1..18
<223> 99-15695.pu

<220>
<221> primer_bind
<222> 481..500
<223> 99-15695.rp complement

<400> 60

```
atcagccttt gtgaggagga ggccctgcct gctctcctcc tgagctgatg ggtcagtcac    60
accaggacaa aggtctgccc ggggctgtgt gggttcctcc ttcctgagct gcacaccagc   120
atctgctgaa caccttctgg agctcagctc agtgtctcgt ccagagacac tggttccctt   180
ggcttctcag caactctcgg atctgggcct gggtctaacc tcagcggtgg tcttgcccat   240
ttctagggcc tcacaattca gcctcatgtc ttcacctgtg gctcttttgc aaggctcaga   300
aagctctagg gtcagttcca gatgactccc accagcatgc cagtaggagc caccaccccc   360
tctcagccag cgccaccata ttccaggcaa attccaactg acacagactt caaggaacga   420
```

61

```
ttgtagcygt tgttcttgct tcttccaaat ggaagagtgc attattgggg tcccttctag      480
cacgcatttc attccccacc                                                  500


<210> 61
<211> 472
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 310
<223> 99-15703-310 : polymorphic base C or T

<220>
<221> misc_binding
<222> 287..333
<223> 99-15703-310.probe

<220>
<221> primer_bind
<222> 291..309
<223> 99-15703-310.mis

<220>
<221> primer_bind
<222> 311..329
<223> 99-15703-310.mis complement

<220>
<221> primer_bind
<222> 1..18
<223> 99-15703.pu

<220>
<221> primer_bind
<222> 452..472
<223> 99-15703.rp complement

<400> 61
agggctttgg gttataggcg ctgaatttct tctaaagcta acctgactct gatgctagaa       60
gagcccattt aaggaaagaa aaacactttt cattgctcga tcaaagttca tccattttgg      120
aaaagacatc aaaccaagtg tgtgacacca ggcacccata tccttcctct ttcccaccac      180
cccacccctg tcctcagggc agtgacagtg aagcctggtg caggtcccgc tgctgctttt      240
tgaagtggca catgctttat tttcttaaaa agaagtgaga gacaacctat gctacaggag      300
gctctgtgay gtttttctga agtacaaccc cttgctctgc caggcagct gtaaagggtc      360
taaagagccc tgagaaagga gagaggattt gggaagccga ggaggcagag ggagaccaca      420
tagcacatgg agttctgaaa gggcccaagt ggagacagaa aacgagtcat gt             472


<210> 62
<211> 470
<212> DNA
<213> Homo sapiens

<220>
```

<221> allele
<222> 400
<223> 99-15870-400 : polymorphic base A or G

<220>
<221> misc_binding
<222> 377..423
<223> 99-15870-400.probe

<220>
<221> primer_bind
<222> 381..399
<223> 99-15870-400.mis

<220>
<221> primer_bind
<222> 401..419
<223> 99-15870-400.mis complement

<220>
<221> primer_bind
<222> 1..21
<223> 99-15870.pu

<220>
<221> primer_bind
<222> 452..470
<223> 99-15870.rp complement

<400> 62
gctcaaatgt atcaaacaca gtttctgtgg tcaagttcct ctccttttct aaatttgctt   60
agaggatctc ataaaacgta actcctctga caagggaacc attttagcac caacactgca   120
aaagcttctg tgttcctaag ggaaagatcc tttcctgaat taaatttaac ctctttagta   180
ctcccattta gccacctgat aaatccactt gagctatctt ttgggaagag agaggtatct   240
gggaacaata acacttcctt tttgaacagt ttaataaagc tttgtgagat ttcaagatga   300
aagataatgt gtaatgctga tagtgccctc caaggctctg cattcatgga tccaattacg   360
tttttgtca tggtaaaagc cacagtggat atattaaatr agagtgtggt ttaagaatga   420
aggcccagga gtctggagat ctggtttcta aggctgactt cacttctgct   470

<210> 63
<211> 469
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 287
<223> 99-16321-287 : polymorphic base A or C

<220>
<221> misc_binding
<222> 264..310
<223> 99-16321-287.probe

63

```
<220>
<221> primer_bind
<222> 268..286
<223> 99-16321-287.mis

<220>
<221> primer_bind
<222> 288..306
<223> 99-16321-287.mis complement

<220>
<221> primer_bind
<222> 1..20
<223> 99-16321.pu

<220>
<221> primer_bind
<222> 451..469
<223> 99-16321.rp complement

<400> 63
ctttaggaat atcccttctg atttgaacaa cattttgcta tccaagttct gtctactttt      60
ttaacaagtt cttgctccgt gtgtctcctt ttgcttgttc tcaagtaagg gagtaacagg     120
gataaactcc cactccttgg taaatctttc tatcattttt ggaaatctca tccattgtag     180
taaatgctct taaatcttca tcttcaggcc gtgacttcca tctagcctcc attcacgttt     240
ccgggtttat gtctgcaatg agcattccgt ggctctacat agatgcmcca ccatacctag     300
aacccatgta tcccaaactc aattctttct ttcccaggac attacttcct gcacttcctt     360
agtctatcaa tggcactgtt attctcttga ccatctagac ttgaaatttt ggggtttgga     420
ctcctcctgc tcccttgctt tatatgtaat cagacatcaa gtctcaatc                 469
```

B'
cont

```
<210> 64
<211> 544
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 194
<223> 99-16333-194 : polymorphic base A or G

<220>
<221> misc_binding
<222> 171..217
<223> 99-16333-194.probe

<220>
<221> primer_bind
<222> 175..193
<223> 99-16333-194.mis

<220>
<221> primer_bind
<222> 195..213
<223> 99-16333-194.mis complement
```

```
<220>
<221> primer_bind
<222> 1..19
<223> 99-16333.pu

<220>
<221> primer_bind
<222> 524..544
<223> 99-16333.rp complement

<400> 64
atttaccccg tctgccttgc aatttcagga tcagtataca tcaaatcaag tgaacaaccc      60
agggaattct gccgttacct tttagaaaca gaataaatat taacagagct ttacttcttt     120
ccaccaagga ggactatatg ttaatacagt aatttacact ggaaaaaata taaatgaaag     180
ggtttagaac ctcrtaactt taaaaataac ataattcctc ctagaacatt cctttcactt     240
gtgattctca aagcactttg catttcccag ctattggcag ggctggaatt aggatcaaag     300
tatcactaaa tggtaggtga aataaatgtg aagctgattt tcaggagtac aggaatggag     360
tcatcaggcg actttaaagt taagaatctg ttggagcagc tgccaataaa tcaaggccca     420
aaggagaaag ttctttggaa accttgaaat attgtataca tttagataat tattgttgtt     480
gtcaatgtta acgaaaaag caataaatca gggagatggc actgatgagt gaggagaaat     540
agac                                                                  544

<210> 65
<211> 475
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 149
<223> 99-5873-159 : polymorphic base C or T

<220>
<221> misc_binding
<222> 126..172
<223> 99-5873-159.probe

<220>
<221> primer_bind
<222> 130..148
<223> 99-5873-159.mis

<220>
<221> primer_bind
<222> 150..168
<223> 99-5873-159.mis complement

<220>
<221> primer_bind
<222> 1..18
<223> 99-5873.pu

<220>
```

65

```
<221> primer_bind
<222> 457..475
<223> 99-5873.rp complement


<220>
<221> misc_feature
<222> 409
<223> n=a, g, c or t


<400> 65
gcgtaacaat aagcagggtt agtcgccaca aaacttgaga taagaggaaa actaaaaaag      60
tctaatgaaa tcagtagtct taaaaagatg acatgatagg aagagaagtg ttaaaaaaga     120
aaaaaaatag gtatgaaaga gagtaacaya taccggaaaa gggataaaat acatcctttg     180
aaagaacaaa gagttattca aattgaattc ttaatgaatt acttaaacag cagattagat     240
attgttaaaa agaggaatag ggaattaaat gatatatgtg atgatattac ctagtgtaac     300
catcaaagat gtattgcaaa tgataaagaa aaaaatgctg ccatggcaat attaatatca     360
taaaaatata ctttaagaag taaataaatg caactaggaa tagagaaans dvhatgaata     420
ataatattta amaaavvgta taacaagtat acataagatg taatatccta aaccg          475

<210> 66
<211> 511
<212> DNA
<213> Homo sapiens


<220>
<221> allele
<222> 49
<223> 99-5912-49 : polymorphic base A or G


<220>
<221> misc_binding
<222> 26..72
<223> 99-5912-49.probe


<220>
<221> primer_bind
<222> 30..48
<223> 99-5912-49.mis


<220>
<221> primer_bind
<222> 50..68
<223> 99-5912-49.mis complement


<220>
<221> primer_bind
<222> 11..31
<223> 99-5912.pu


<220>
<221> primer_bind
<222> 494..511
<223> 99-5912.rp complement
```

<400> 66
```
aaatataata gtcaaatcat gttaccatta ggacacatta aaaatgtcra attaccttgg        60
gaccttatat gaacatatta agataataat gatagtgttc agtgcaatat tcagatcaat       120
agtttaaacc caaaatattt ataccttcag attagatgta tgcaaatgca ttgattcatg       180
tgtctttat ctgttgttta catttggaga aatatttgag aaatatttca aaatggaatt        240
tatataaatt taaacacata atggttttat gtaaaaatat tgctaaatta cattttcccc       300
ttaattctta tttcttggaa acgtgcctta gtcgctgaaa tattcataca ttaacacaat       360
gaaagaagtg aaccttacta ggctttgact atcaggtttg ctgttggttt ttgactattg       420
tgaaactata gcctgatttc taaatcagga agaaacgtgt attgttgtta atatggacac       480
atgacatatt tgtctgcctg acttttgatc c                                      511
```

<210> 67
<211> 485
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 210
<223> 99-6012-220 : polymorphic base G or T

<220>
<221> misc_binding
<222> 187..233
<223> 99-6012-220.probe

<220>
<221> primer_bind
<222> 191..209
<223> 99-6012-220.mis

<220>
<221> primer_bind
<222> 211..229
<223> 99-6012-220.mis complement

<220>
<221> primer_bind
<222> 1..19
<223> 99-6012.pu

<220>
<221> primer_bind
<222> 467..485
<223> 99-6012.rp complement

<400> 67
```
gtcttgactt gttttcctga gggtccaggt tgatttgcat gctcttgagg aaatatacac        60
gtcttctcag ttttaataat tgactgacag ccctgtggtt tctcaggacc cagtgagctg       120
ctgctcccag gtcagtctgc aaaggatgct ggttcccttg tggtctcatc aaggtgagga       180
atttcctgat tttagagatt tctttatcck aattttgaag actttctttc acatttctag       240
gcataaaaaa atgtacagca ctctactgct tgtttaacaa atggatagtg atatatctgc       300
caacaaagac cacatggagt atttcattga ctatcagaga agtttcctcg aaaggcacca       360
tacttagtgt tttatttcca tgagtgaagg aaaattagtt atttgaagta tttggctgtc       420
```

```
tttagttgtt tctaaagtag tgctgatttt atatgcccat aatattcata tatacaccca    480
ggata                                                                485
```

<210> 68
<211> 529
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 89
<223> 99-6080-99 : polymorphic base C or T

<220>
<221> misc_binding
<222> 66..112
<223> 99-6080-99.probe

<220>
<221> primer_bind
<222> 70..88
<223> 99-6080-99.mis

<220>
<221> primer_bind
<222> 90..108
<223> 99-6080-99.mis complement

<220>
<221> primer_bind
<222> 1..18
<223> 99-6080.pu

<220>
<221> primer_bind
<222> 509..529
<223> 99-6080.rp complement

<400> 68
```
aaatgtgtcc ctgaaaccca tgctatattc aactgaatat tctaatgtct ttgattacaa     60
agccatctct agcaatttaa tacaattayg aaatggaaaa gttggcaaat gcaaaacaat    120
agctcgtgtt caaggtatgt ctttattagg ggaagtttat cgaaacagat gtttatgcta    180
tttcctataa actagattct aaaatatttt attctataaa gatgtattga ctttatatga    240
aaaaattatt gaaaaatcta caagatggtg aaactcttta gaactatatt tctattacaa    300
gtttattttt aatttcaaaa atgtactgca taaatgcagc aaaaccttta ttgtcacata    360
ttaaaacatg tacattattg tgtgcaaatt aaaatttcat taccttaaac caaaaagtga    420
gttggccaga tagtaaataa tttaggctct aaggctgaaa agcgcttgta ttaattactc    480
aactccacca ctattttgcc aaagcagtca cagacaatac gcattcaca                529
```

<210> 69
<211> 489
<212> DNA
<213> Homo sapiens

<220>
<221> allele
<222> 156
<223> 99-7308-157 : polymorphic base C or T

<220>
<221> misc_binding
<222> 133..179
<223> 99-7308-157.probe

<220>
<221> primer_bind
<222> 137..155
<223> 99-7308-157.mis

<220>
<221> primer_bind
<222> 157..175
<223> 99-7308-157.mis complement

<220>
<221> primer_bind
<222> 1..18
<223> 99-7308.pu

<220>
<221> primer_bind
<222> 469..489
<223> 99-7308.rp complement

<400> 69
tgtggtctgg atatggtgra ctgtccttca cacacagatg tgggaagcca tgatcatcag   60
ttgcattatt cctgaggggc aatgcattcc agttacatag aaccagtttc tacgtttcag   120
ggtatatgta ttcatggtga caaatttatt cacatyttaa gtaattttaa gtaattcaca   180
ttttaagtaa ttttcctgaa tgtgcctcat tggcttctgt gcctcttcag aaaagatgaa   240
ctaaacactg gcatatgtgt tcagatttca acattccgtt gttttcattg tggataattt   300
ctgtcccata tttttgtgta aagttagaca ataaagtgtt aatattctgg cgtcggcaca   360
ttttctttcc tgataaataa caattcacat atcttttttaa aatatcagag aatatagtaa   420
ccaatttcca attctttttt caccatgtat ctattggagt tttaaaatga ctaatactaa   480
ggcaactat   489

<210> 70
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> sequencing oligonucleotide PrimerPU

<400> 70
tgtaaaacga cggccagt   18

<210> 71
<211> 18

69

```
<212> DNA
<213> Artificial Sequence

<220>
<223> sequencing oligonucleotide PrimerRP

<400> 71
caggaaacag ctatgacc                                              18
```